



1

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10/588,114

<141> 2006-07-27

<150> PCT/US05/002633

<151> 2005-01-28

<150> 60/628,997

<151> 2004-11-18

<150> 60/607,684

<151> 2004-09-07

<150> 60/557,152

<151> 2004-03-26

<150> 60/539,774

<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide linker

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Gly Ser Gly Gly Gly
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<210> 2

<211> 37

<212> PRT

<213> Homo sapiens

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Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
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Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
35

<210> 3
<211> 14
<212> PRT
<213> Rous sarcoma virus

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Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
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<213> Unknown

<220>
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sequence

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Asp Ser Glu Glu Glu Leu Pro Thr Arg
20 25

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<212> PRT
<213> Monkey virus SV40

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Pro Lys Lys Lys Lys Lys Val
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<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

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Ala Arg Arg Arg Arg Pro
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<210> 7
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<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: NF kappa-B p50
sequence

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Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
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<210> 8

<211> 9

<212> PRT

<213> Unknown

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<223> Description of Unknown: NF kappa-B p65
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<210> 9

<211> 21

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: Nucleoplasmin
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Ala Val Lys Arg Pro Ala Ala Thr Leu Lys Lys Ala Gly Gln Ala Lys
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Lys Lys Lys Leu Asp
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<210> 10

<211> 5

<212> PRT

<213> Homo sapiens

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Lys Phe Glu Arg Gln
1 5

<210> 11

<211> 36

<212> PRT

<213> Homo sapiens

<400> 11

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
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Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
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Tyr Gln Thr Ile
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<210> 12
 <211> 35
 <212> PRT
 <213> Homo sapiens

<400> 12
 Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
 1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
 20 25 30

Glu Gln Phe
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<210> 13
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 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 13
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Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
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<210> 14
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 <213> Saccharomyces cerevisiae

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Thr Leu Cys Ser Ser Arg Tyr Leu Leu
 20 25

<210> 15
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 <213> Saccharomyces cerevisiae

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 1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
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 35 40 45
 Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
 50 55 60

<210> 16
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 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
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 <213> Unknown

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 reticulum localizing sequence

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<210> 18
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 <213> Human adenovirus type 19

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<210> 19
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 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown: Interleukin-2
sequence

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Val Thr Asn Ser
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<210> 20

<211> 29

<212> PRT

<213> Homo sapiens

<400> 20

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1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 21

<211> 27

<212> PRT

<213> Homo sapiens

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Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
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Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
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<210> 22

<211> 18

<212> PRT

<213> Influenza A virus

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Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
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Gln Ile

<210> 23

<211> 24

<212> PRT

<213> Unknown

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<223> Description of Unknown: Interleukin-4
sequence

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Cys Ala Gly Asn Phe Val His Gly
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<212> DNA

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<223> Description of Artificial Sequence: Synthetic
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<210> 26

<211> 18

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<223> Description of Artificial Sequence: Synthetic
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<210> 27

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<212> DNA

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<220>

<223> Description of Artificial Sequence: Synthetic primer

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<210> 35

<211> 1995

<212> DNA

<213> Escherichia coli

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<210> 36

<211> 664

<212> PRT

<213> Escherichia coli

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10

15

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Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu		
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His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly		
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Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn		
	130					135					140						
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Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly		
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Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu		
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Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn		
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 Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
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 Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
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 Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
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 Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
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 Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
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 Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
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 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
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 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
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 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
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 595 600 605
 Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met
 610 615 620

Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala
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<213> Escherichia coli

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<210> 38
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<212> PRT
<213> Escherichia coli

<400> 38

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Val	Gly 50	Lys	Lys	Phe	Glu	Lys 55	Asp	Thr	Gly	Ile	Lys 60	Val	Thr	Val	Glu
His 65	Pro	Asp	Lys	Leu	Glu 70	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly 80
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Asp	Lys	Leu 115	Tyr	Pro	Phe	Thr	Trp 120	Asp	Ala	Val	Arg	Tyr 125	Asn	Gly	Lys
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Tyr	Ala	Phe 195	Lys	Tyr	Glu	Asn	Gly 200	Lys	Tyr	Asp	Ile	Lys 205	Asp	Val	Gly
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Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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Gln Thr Arg Ile Thr Lys
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<210> 39

<211> 1983

<212> DNA

<213> Escherichia coli

<400> 39

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1983

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 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
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 115 120 125
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 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
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 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
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 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

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Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
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Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	385	390	395
Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	405	410	415
Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	420	425	430
Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	435	440	445
Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	450	455	460
Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	465	470	475
Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	485	490	495
Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	500	505	510
Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	515	520	525
Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	530	535	540
Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	545	550	555
Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	565	570	575

Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp
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His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ala
595 600 605

Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro
610 615 620

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala
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<212> DNA
<213> Escherichia coli

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1986

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 <211> 661
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Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
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<211> 666

<212> PRT

<213> Escherichia coli

<400> 44

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Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
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Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
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Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
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Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asn Glu
 210 215 220

Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala
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Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	
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Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	
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Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	
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Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	
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Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	
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			340					345					350			
Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	
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Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	
	370					375					380					
Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	
385					390					395					400	
Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	
				405					410					415		
Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	
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Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	
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Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	
	450					455					460					
Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	Arg	
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Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Val	Asp	Leu	Ile	Lys	
				485					490					495		
Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	
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Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	
		515					520					525				
Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	
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Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala
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Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu
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Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp
580 585 590

Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala
595 600 605

Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu
610 615 620

Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg
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Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala
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Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
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<210> 45

<211> 1989

<212> DNA

<213> Escherichia coli

<400> 45

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<210> 46
<211> 662
<212> PRT
<213> Escherichia coli

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      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
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Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
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Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val		260	265				270	
Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala		275	280				285	
Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala		290	295				300	
Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr		305	310				315	320
Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile		325	330				335	
Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu		340	345				350	
Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr		355	360				365	
Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro		370	375				380	
Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly		385	390				395	400
Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg		405	410				415	
Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu		420	425				430	
Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala		435	440				445	
Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile		450	455				460	
Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His		465	470				475	480
Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	His	Met		485	490				495	
Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly		500	505				510	
Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp		515	520				525	

Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly
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 Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala
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 Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu
 565 570 575
 Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly
 580 585 590
 Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg
 595 600 605
 Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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 Gln Thr Arg Ile Thr Lys
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 <211> 1989
 <212> DNA
 <213> Escherichia coli

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<210> 48

<211> 662

<212> PRT

<213> Escherichia coli

<400> 48

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Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
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Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115                      120                      125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130                      135                      140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145                      150                      155                      160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
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Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180                      185                      190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195                      200                      205

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Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
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Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
		275					280					285			
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
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Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn
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Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu
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Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala
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Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg
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Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser
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Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu
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Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys
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Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
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Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
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Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
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Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
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Gln Thr Arg Ile Thr Lys
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tctcagaatg acttggttga gtactcacca gtcacagaaa agcatcttac ggatggcatg 1680
acagtaagag aattatgcag tgctgccata accatgagtg ataacactgc ggccaactta 1740
cttctgacaa cgatcggagg accgaaggag ctaaccgctt ttttgacaaa catgggggat 1800
catgtaactc gccttgatcg ttgggaaccg gaactgaatg aagccgccgc caccatggaa 1860
aacgcccgaga aaggtgaaat catgccgaac atccgcgaga tgtccgcttt ctggtatgcc 1920
gtgcgtactg cggatgatcaa cgccgccagc ggtcgtcaga ctgtcgatga agccctgaaa 1980
gacgcgcaga ctcgatcac caagtaa                                2007

```

<210> 50

<211> 668

<212> PRT

<213> *Escherichia coli*

<400> 50

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
                20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
    35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
    50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
    65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
    85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
    100                      105                      110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
    115                      120                      125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
    130                      135                      140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
    145                      150                      155                      160

```

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
    165                      170                      175

```

```

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
    180                      185                      190

```


Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Asn Glu Ala Ile Pro Asn
 340 345 350
 Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg
 355 360 365
 Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu
 370 375 380
 Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser
 385 390 395 400
 Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu
 405 410 415
 Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro
 420 425 430
 Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp
 435 440 445
 Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His
 450 455 460
 Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu
 465 470 475 480
 Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser
 485 490 495

Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met
 500 505 510
 Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp
 515 520 525
 Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp
 530 535 540
 Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met
 545 550 555 560
 Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr
 565 570 575
 Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr
 580 585 590
 Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp
 595 600 605
 Glu Pro Glu Leu Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys
 610 615 620
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 625 630 635 640
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 645 650 655
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 660 665

<210> 51
 <211> 1989
 <212> DNA
 <213> Escherichia coli

<400> 51
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 aaaggctata acggtctcgc tgaagtccgt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcggtatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgctggat aacgctggcg cgaaagcggg tctgaccttc 660
 ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaaa 720
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
 atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
 ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggctctgga agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgc agcaatggca 1080

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acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta 1140
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc ctttccggct 1200
ggctgggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca 1260
gcactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag 1320
gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tgggacaaga gccacccaga aacgctggtg aaagtaaaag atgctgaaga tcagttgggt 1440
gcacgagtgg gttacatcga actggatctc aacagcggta agatccttga gagttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagttc tgctatgtgg cgcggtatta 1560
tcccgtgttg acgccgggca agagcaactc ggtcgcgcga tacactattc tcagaatgac 1620
ttggttgagt actcaccagt cacagaaaag catcttaagg atggcatgac agtaagagaa 1680
ttatgcagtg ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg 1740
atcgaggagc cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcggt gggaaccgga actgaatgaa gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

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<210> 52
 <211> 662
 <212> PRT
 <213> Escherichia coli

<400> 52
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 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu	Gln	Glu	Pro 180	Tyr	Phe	Thr	Trp	Pro 185	Leu	Ile	Ala	Ala	Asp 190	Gly	Gly
Tyr	Ala	Phe 195	Lys	Tyr	Glu	Asn	Gly 200	Lys	Tyr	Asp	Ile	Lys 205	Asp	Val	Gly
Val	Asp 210	Asn	Ala	Gly	Ala	Lys 215	Ala	Gly	Leu	Thr	Phe 220	Leu	Val	Asp	Leu
Ile 225	Lys	Asn	Lys	His	Met 230	Asn	Ala	Asp	Thr	Asp 235	Tyr	Ser	Ile	Ala	Glu 240
Ala	Ala	Phe	Asn	Lys 245	Gly	Glu	Thr	Ala	Met 250	Thr	Ile	Asn	Gly	Pro 255	Trp
Ala	Trp	Ser	Asn 260	Ile	Asp	Thr	Ser	Lys 265	Val	Asn	Tyr	Gly	Val 270	Thr	Val
Leu	Pro	Thr 275	Phe	Lys	Gly	Gln	Pro 280	Ser	Lys	Pro	Phe	Val 285	Gly	Val	Leu
Ser	Ala 290	Gly	Ile	Asn	Ala	Ala 295	Ser	Pro	Asn	Lys	Glu 300	Leu	Ala	Lys	Glu
Phe 305	Leu	Glu	Asn	Tyr	Leu 310	Leu	Thr	Asp	Glu	Gly 315	Leu	Glu	Ala	Val	Asn 320
Lys	Asp	Lys	Pro	Leu 325	Gly	Ala	Val	Ala	Leu 330	Lys	Ser	Tyr	Glu	Glu 335	Glu
Leu	Ala	Lys	Asp 340	Pro	Arg	Asn	Glu	Ala 345	Ile	Pro	Asn	Asp	Glu 350	Arg	Asp
Thr	Thr	Met 355	Pro	Ala	Ala	Met	Ala 360	Thr	Thr	Leu	Arg	Lys 365	Leu	Leu	Thr
Gly	Glu 370	Leu	Leu	Thr	Leu	Ala 375	Ser	Arg	Gln	Gln	Leu 380	Ile	Asp	Trp	Met
Glu 385	Ala	Asp	Lys	Val	Ala 390	Gly	Pro	Leu	Leu	Arg 395	Ser	Ala	Leu	Pro	Ala 400
Gly	Trp	Phe	Ile	Ala 405	Asp	Lys	Ser	Gly	Ala 410	Gly	Glu	Arg	Gly	Ser 415	Arg
Gly	Ile	Ile	Ala 420	Ala	Leu	Gly	Pro	Asp 425	Gly	Lys	Pro	Ser	Arg 430	Ile	Val
Val	Ile	Tyr 435	Thr	Thr	Gly	Ser	Gln 440	Ala	Thr	Met	Asp	Glu 445	Arg	Asn	Arg
Gln	Ile	Ala	Glu	Ile	Gly	Ala 455	Ser	Leu	Ile	Lys	His 460	Trp	Asp	Lys	Ser
His 465	Pro	Glu	Thr	Leu	Val 470	Lys	Val	Lys	Asp	Ala 475	Glu	Asp	Gln	Leu	Gly 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
500 505 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 53

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 53

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tttggtata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttta tgcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtgag agcgcgctga tggtcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cggtcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660

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ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atgggtccaac 780
atcgacacca gcaaagtga ttatgggtgta acggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca cttctgcgt cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cacttttaaa gttctgctat gtggcgcggt attatcccgt 1560
gttgacgcgc ggcaagagca actcgggtcgc cgcatacact attctcagaa tgacttggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtcgcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcccga gaaaggtgaa 1860
atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

```

<210> 54

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 54

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1              5              10              15
Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30
Leu Val Ile Trp Ile Asn Gly Leu Phe Gly Tyr Asn Gly Leu Ala Glu
      35              40              45
Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60
His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80
Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95
Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110
Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

```

Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	
	130					135					140					
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	
145					150					155					160	
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	
				165					170					175		
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	
			180					185						190		
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	
		195					200						205			
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	
	210					215					220					
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	
225					230					235					240	
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	
			245						250					255		
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	
			260					265					270			
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	
		275					280					285				
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	
	290					295					300					
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	
305					310					315					320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	
				325					330					335		
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	
			340					345					350			
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	
		355					360					365				
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	
	370					375					380					
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	
385					390					395					400	
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	
				405					410					415		
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	
			420					425					430			

[illegible]

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<210> 55
<211> 662
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 55
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Leu Gln Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Gln Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
 565 570 575
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605
 Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 56
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 56
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gagggctata acgggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgttg agcatccgga taaactggaa gagaaattcc cacagggtgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgcccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg ggcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcgaaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcgggtta 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgccca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
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aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccg 1560
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gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtgcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgga 1740
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cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

<210> 57
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 57
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 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Lys Glu Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Arg Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val		
			260					265					270				
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu		
		275					280					285					
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu		
	290					295					300						
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn		
305					310					315					320		
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu		
				325					330					335			
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr		
			340					345					350				
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu		
		355					360					365					
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala		
	370					375					380						
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp		
385					390					395					400		
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile		
				405					410					415			
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile		
			420					425					430				
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile		
		435					440					445					
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro		
	450					455					460						
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg		
465					470					475					480		
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser		
				485				490						495			
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu		
			500					505					510				
Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu		
		515					520					525					
Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro		
	530					535					540						
Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys		
545					550					555					560		

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 58

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 58

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gagggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg tgcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtcg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcc aaccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cgataaaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggcgacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacggtttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccg 1560

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gttgacgccg ggcaagagca actcgggtcgc cgcatacaact attctcagaa tgacttgggtt 1620
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agtgtgtcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcggg 1740
ggaccgaagg agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccgc gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa                                     1989

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<210> 59
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 59
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Leu Glu Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Arg Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu
210						215					220				
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu
225					230					235					240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp
				245					250					255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
			260					265					270		
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
		275					280					285			
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
	290					295					300				
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn
305					310					315					320
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu
				325					330					335	
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr
			340					345					350		
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu
		355					360					365			
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala
	370					375					380				
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp
385					390					395					400
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile
				405					410					415	
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile
			420					425					430		
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile
		435					440					445			
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro
	450					455					460				
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg
465					470					475					480
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser
				485					490					495	
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu
			500					505					510		

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
515 520 525

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
530 535 540

Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 60

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 60

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aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgctggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020

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```

ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggtatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcggtgg ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cagcagtggtg ttacatcgaa ctggatctca acagcggtaa gacccctgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc 1380
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gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
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gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgccctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccctt tccggtggtg tccgccacca tggaaaacgc ccagaaaggt 1860
gaaatcatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

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<210> 61

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 61

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10          15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25          30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40          45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55          60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70          75          80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90          95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                     105          110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115                     120          125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130                     135          140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145                     150          155          160

```

Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	
				165					170					175		
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	
			180					185					190			
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	
		195					200					205				
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	
	210					215					220					
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	
225					230					235					240	
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	
			245						250					255		
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	
			260					265					270			
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	
		275					280					285				
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	
	290				295						300					
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	
305					310					315					320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	
			325						330					335		
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	
		340					345						350			
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	
		355					360					365				
Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	
	370					375					380					
Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	
385					390					395					400	
His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	
			405						410					415		
Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	
			420					425					430			
Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	
		435					440					445				
Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	
	450					455						460				

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro
610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
645 650 655

Ala Gln Thr Arg Ile Thr Lys
660

<210> 62

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 62

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tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccaac cgcgcaaaaa cctgggaaga gatccccggc 480
```

```

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccgtgggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggtcaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggctctga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgtcgaga taggtgcctc actgattaag 1200
cattggggat ccggcgggtg ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cagcagtggtg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcaact ttaaagtctt gctatgtggc 1380
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcggtg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccct tccggtggtg tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgcgc ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 63

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 63

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1             5             10             15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20             25             30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35             40             45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50             55             60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65             70             75             80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85             90             95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

```

Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	340	345	350
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	355	360	365
Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	370	375	380
Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	385	390	395
His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	405	410	415

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro
 610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
 625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
 645 650 655

Ala Gln Thr Arg Ile Thr Lys
 660

<210> 64

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 64

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atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
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aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gattgggtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcggtatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaaaggttaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaa agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttac aggaagagtt ggcgaaagat 1020
ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
gcagcaactg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcgtggt ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcgttaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagtctt gctatgtggc 1380
gcggtattat ccggtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccggca acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccct tccggtggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcgtcgc tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 65

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 65

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1             5             10             15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20             25             30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35             40             45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50             55             60

```


His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly	
65					70					75					80	
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr	
				85					90					95		
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln	
			100					105					110			
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Trp	Val	Arg	Tyr	Asn	Gly	Lys	
		115					120					125				
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	
	130					135					140					
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	
145					150					155					160	
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	
				165					170					175		
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	
			180					185					190			
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	
	195						200					205				
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	
	210					215					220					
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	
225					230					235					240	
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	
			245						250					255		
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	
			260					265					270			
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	
		275					280					285				
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	
	290					295					300					
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	
305					310					315					320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	
				325					330					335		
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	
			340					345					350			
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	
		355					360					365				

<210> 66
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 66
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 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttacccga tcgctgttga agcgttatcg 420
 ctggataaag aactgaaagc gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac gggcatctta cggatggcat gacagtaaga 600
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 660
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 720
 cgccttgatc gttgggaacc ggaactgaat gaagccatac caaacgacga gcgtgacacc 780
 acgatgcctg cagcaatggc aacaacgctt cgcaaaactat taactggcga actacttact 840
 ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgc aggaccactt 900
 ctgcgctcgg cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt 960
 gggctctcgg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt 1020
 atctacacga cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata 1080
 ggtgcctcac tgattaagca ttgggacaag agccaccag aaacgctggt gaaagtaaaa 1140
 gatgctgaag atcagttggg tgcacgagtg ggttacatcg aactggatct caacagcggg 1200
 aagatccttg agagttttcg ccccgaagaa cgttttccaa tgatgagcac ttttaaagtt 1260
 ctgctatgtg gcgcggtatt atcccgtgtt gacgcggggc aagagcaact cggtcgccgc 1320
 atacactatt ctacagaatga cttggttgag tactcaccag tcacagacgg gggttatgcg 1380
 ttcaagtatg aaaacggcaa gtacgacatt aaagacgtgg gcgtggataa cgctggcgcg 1440
 aaagcgggtc tgaccttccg ggttgacctg attaaaaaca aacacatgaa tgcagacacc 1500
 gattactcca tcgcagaagc tgcctttaat aaaggcgaaa cagcgatgac catcaacggc 1560
 ccgtgggcat ggtccaacat cgacaccagc aaagtgaatt atggtgtaac ggtactgccg 1620
 accttcaagg gtcaaccatc caaacggtc gttggcgtgc tgagcgcagg tattaacgcc 1680
 gccagtccga acaaagagct ggcgaaagag ttctcgaaaa actatctgct gactgatgaa 1740
 ggtctggaag cggttaataa agacaaaccg ctgggtgccc tagcgtgaa gtcttacgag 1800
 gaagagttgg cgaaagatcc acgtattgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
 atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
 aacgcgcga gcggtcgtca gactgtcgat gaagccctga aagacgcga gactcgtatc 1980
 accaagtaa 1989

<210> 67
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 67
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15

Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys		
			20					25						30			
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu		
		35					40					45					
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu		
	50					55					60						
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly		
	65				70					75					80		
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr		
				85					90					95			
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln		
			100					105					110				
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys		
		115					120					125					
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn		
	130					135					140						
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala		
	145				150					155					160		
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn		
				165				170						175			
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	His		
			180					185					190				
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr		
		195					200					205					
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly		
	210					215					220						
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr		
	225				230					235					240		
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp		
				245					250					255			
Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys		
			260					265					270				
Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile		
		275					280					285					
Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala		
	290					295					300						
Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg		
	305				310					315					320		

Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser		
				325					330					335			
Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu		
			340					345					350				
Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp		
		355					360					365					
Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp		
	370					375					380						
Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly		
385					390					395					400		
Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser		
				405					410					415			
Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala		
			420					425					430				
Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu		
		435					440					445					
Val	Glu	Tyr	Ser	Pro	Val	Thr	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu		
	450					455					460						
Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala		
465					470					475					480		
Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met		
				485					490					495			
Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly		
			500					505					510				
Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp		
		515					520					525					
Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly		
		530				535					540						
Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala		
545					550					555					560		
Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu		
				565					570					575			
Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly		
			580					585					590				
Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg		
		595					600					605					
Ile	Ala	Ala	Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn		
	610					615					620						

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 68
 <211> 1995
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 68
 atgaaaataa aaacagggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggtt agcatccgga taaactggaa gagaaattcc cacagggttg ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
 ctggataaag aactgaaagc gaaaggtaa agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac gggcttctgc gctcggccct tccggtggc 600
 tgggtttatt ctgataaatc tggagccggt gagcgtgggt ctgcggtat cattgcagca 660
 ctggggccag atggtaaagg ctcccgtatc gtagttatct acacgacggg gagtcaggca 720
 actatggatg aacgaaatag acagatcgct gagatagggt cctcactgat taagcattgg 780
 ggatccggcg gtggccaccc agaaacgctg gtgaaagtaa aagatgctga agatcagttg 840
 ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt 900
 cgccccgaag aacgttttcc aatgatgagc acttttaaaag ttctgctatg tggcgcggtg 960
 ttatcccggt ttgacgcggg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat 1020
 gacttgggtg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga 1080
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 1140
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 1200
 cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc 1260
 acgatgcctg cagcaatggc aacaacgttg cgcaaactat taactggcga actacttact 1320
 ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgtg agacgggggt 1380
 tatgcgttca agtatgaaaa cggcaagtac gacattaaag acgtgggctg ggataacgct 1440
 ggcgcgaaa agcgggtctgac cttcctggtt gacctgatta aaaacaaaca catgaatgca 1500
 gacaccgatt actccatcgc agaagctgcc tttaataaaag gcgaaacagc gatgaccatc 1560
 aacggcccggt gggcatggtc caacatcgac accagcaaaag tgaattatgg tgtaacggta 1620
 ctgcccacct tcaaggttca accatccaaa ccgttcgttg gcgtgctgag cgcagggtatt 1680
 aacgcccga gtccgaacaa agagctggcg aaagagttcc tcgaaaacta tctgctgact 1740
 gatgaagggtc tggaagcgggt taataaagac aaaccgctgg gtgccgtagc gctgaagtct 1800
 tacgaggaag agttggcgaa agatccacgt attgccgcca ccatggaaaa cgcccagaaa 1860
 ggtgaaatca tgccgaacat cccgcagatg tccgctttct ggtatgccgt gcgtactgcg 1920
 gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980
 cgtatcacca agtaa 1995

<210> 69
 <211> 664
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 69
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Leu
 180 185 190
 Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly
 195 200 205
 Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp
 210 215 220
 Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala
 225 230 235 240
 Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu
 245 250 255

Ile	Lys	His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	260	265	270	
Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	275	280	285	
Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	290	295	300	
Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	305	310	315	320
Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	325	330	335	
Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	340	345	350	
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	355	360	365	
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	370	375	380	
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	385	390	395	400
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp	405	410	415	
Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	420	425	430	
Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	435	440	445	
Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	450	455	460	
Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	465	470	475	480
Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	485	490	495	
His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	500	505	510	
Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	515	520	525	
Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	530	535	540	
Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	545	550	555	560


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<210> 70
<211> 2004
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide construct
```

<400>	70						
atgaaaataa	aaacaggtgc	acgcattcctc	gcattatccg	cattaacgac	gatgatgttt	60	
tccgcctcgg	ctctcgccaa	aatcgaagaa	ggtaaactgg	taatctggat	taacggcgat	120	
aaaggctata	acggtctcgc	tgaagtcggt	aagaaattcg	agaaagatac	cggaattaaa	180	
gtcaccgttg	agcatccgga	taaactggaa	gagaaattcc	cacaggttgc	ggcaactggc	240	
gatggccctg	acattatctt	ctgggcacac	gaccgctttg	gtggctacgc	tcaattctggc	300	
ctggttggtc	aaatcacccc	ggacaaagcg	ttccaggaca	agctgtatcc	gtttacctgg	360	
gatgccgtac	gttacaacgg	caagctgatt	gcttaccoga	tcgctgttga	agcgttatcg	420	
ctgatttata	acaaagatct	gctgccgaac	ccgccaaaaa	cctgggaaga	gatcccggcg	480	
ctggataaaag	aactgaaagc	gaaaggtaag	agcgcgctga	tgttcaacct	gcaagaaccg	540	
tactttcacct	ggccgctgat	tgctgctgac	gggaatgaag	ccataccaaa	cgacgagcgt	600	
gacaccacga	tgcttcgagc	aatggcaaca	acgttgcgca	aactattaac	tggcgaaacta	660	
cttactctag	cttcccgcga	acaattaata	gactggatgg	aggcggataa	agttgcagga	720	
ccactttctgc	gctcggccct	tccggctggc	tggtttattg	ctgataaaatc	tggagccggt	780	
gagcgtgggt	ctcgcggtat	cattgcagca	ctggggccag	atggtaagcc	ctcccgtatc	840	
gtagttatct	acacgacggg	gagtcaggca	actatggatg	aacgaaatag	acgatctgct	900	
gagataagtg	ctcactgat	taagcattgg	gacaagagcc	accagaaaac	cggtggtgaa	960	
gtaaaagatg	ctgaagatca	gttgggtgca	cgagtgggtt	acatcgaact	ggatctcaac	1020	
agcggtaaga	tccttgagag	ttttcgcccc	gaagaacggt	ttccaatgat	gagcactttt	1080	
aaagttctgc	tatgtggcgc	ggtattatcc	cgtgttgacg	ccgggcaaga	gcaactcggt	1140	
cgccgcatac	actattctca	gaatgacttg	gttgagtact	caccagtcac	agaaaagcat	1200	
cttacggatg	gcatgacagt	aagagaatta	tgcagtgctg	ccataaccat	gagtgataac	1260	
actgcggcc	acttacttct	gacaacgatc	ggaggaccga	aggagctaac	cgcttttttg	1320	
cacaacatgg	gggatcatgt	aactcgcctt	gatcgttggg	aaccggaact	gaaatgaagcc	1380	
gacgggggtt	atgcgttcaa	glatgaaaac	ggcaagtacg	acattaaaaga	cgtggcgctg	1440	
gataacgctg	gcgcgaaagc	gggtctgacc	ttcctggttg	acctgattaa	aaacaaacac	1500	
atgaatgcaq	acaccgatta	ctccatcgca	gaagctgcct	ttaataaaagg	cgaaacagcg	1560	

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atgaccatca acggcccgtg ggcattgtcc aacatcgaca ccagcaaagt gaattatggt 1620
gtaacgggtac tgccgacctt caagggtcaa ccatccaaac cgttcgttgg cgtgctgagc 1680
gcaggtatta acgcccgcag tccgaacaaa gagctggcga aagagttcct cgaaaactat 1740
ctgctgactg atgaagggtt ggaagcgggt aataaagaca aaccgctggg tgccgtagcg 1800
ctgaagtctt acgaggaaga gttggcgaaa gatccacgta ttgccgccac catggaaaac 1860
gcccagaaaag gtgaaatcat gccgaacatc ccgcagatgt ccgctttctg gtatgccgtg 1920
cgtactgctg tgatcaacgc cgccagcggg cgtcagactg tcgatgaagc cctgaaagac 1980
gcgcagactc gtatcaccaa gtaa                                     2004

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<210> 71

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 71

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115                      120                      125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130                      135                      140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145                      150                      155                      160

```

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165                      170                      175

```

```

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Asn
      180                      185                      190

```

```

Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met
      195                      200                      205

```

Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	210	215	220	
Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	225	230	235	240
Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	245	250	255	
Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	260	265	270	
Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	275	280	285	
Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	290	295	300	
Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	305	310	315	320
Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	325	330	335	
Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	340	345	350	
Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	355	360	365	
Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	370	375	380	
Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	385	390	395	400
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	405	410	415	
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	420	425	430	
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	435	440	445	
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Asp	Gly	Gly	Tyr	450	455	460	
Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	465	470	475	480
Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	485	490	495	
Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	500	505	510	

Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala
515 520 525

Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu
530 535 540

Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser
545 550 555 560

Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe
565 570 575

Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys
580 585 590

Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu
595 600 605

Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly
610 615 620

Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val
625 630 635 640

Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu
645 650 655

Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
660 665

<210> 72

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 72

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atgaaaataa aaacaggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
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aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaaagc ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tgcgtgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaaaca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020

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ccacgtattg cgcgccaccat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatcccg 1080
cagatgtccg ctttctggta tgccgtgcgt actgcggtga tcaacgccgc cagcgggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtgc cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg ggatcatgta 1320
actcgccttg atcgttggga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
cttctgcgct cggcccttcc ggctggctgg tttattgctg ataaatctgg agccgggtgag 1560
cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgtctgag 1680
ataggtgcct cactgattaa gcattgggga tccggcgtg gccaccaga aacgctggtg 1740
aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcga actggatctc 1800
aacagcggta agatccttga gagttttcgc cccgaagaac gttttccaat gatgagcact 1860
tttaaagttc tgctatgtgg cgcggtatta tcccgtgttg acgccgggca agagcaactc 1920
ggtcgcgcga tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg atggcaagtg a                                     2001

```

<210> 73

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 73

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115                      120                      125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130                      135                      140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145                      150                      155                      160

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val
 385 390 395 400
 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala
 405 410 415
 Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540

Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560

Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro
 565 570 575

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655

Val Thr Glu Lys His Leu Thr Asp Gly Lys
 660 665

<210> 74

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 74

atgaaaataa aaacagggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaacctgg taatctggat taacggcgat 120
 aaaggctata acgggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggttg agcatccgga taaactggaa gagaaattcc cacagggttg gcgaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480

```

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgctggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttgccgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtattg ccgccaccat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatccc 1080
cagatgtccg ctttctggta tgccgtgcgt actgcggtga tcaacgccgc cagcggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtctg cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg ggatcatgta 1320
actcgccttg atcgttgga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
cttctgcgct cggcccttcc ggctggctgg tttattgctg ataaatctgg agccggtgag 1560
cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgtgag 1680
ataggtgcct cactgattaa gcattgggga tccggcggtg gccaccaga aacgctggtg 1740
aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcga actggatctc 1800
aacagcggta agatccttga gagttttcgc cccgaagaac gttttccaat gatgagcact 1860
tttaaagttc tgctatgtgg cgcggtatta tcccggtgtg acgccgggca agagcaactc 1920
ggtcgccgca tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg aagtgaagag cactagttag 2010

```

<210> 75

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 75

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

```


Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	Thr	Met	Glu	Asn	Ala	Gln	Lys	340	345	350
Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln	Met	Ser	Ala	Phe	Trp	Tyr	Ala	355	360	365
Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala	Ser	Gly	Arg	Gln	Thr	Val	Asp	370	375	380
Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Arg	Ile	Thr	Lys	Gly	Met	Thr	Val	385	390	395
Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	405	410	415

Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430

Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445

Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540

Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560

Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro
 565 570 575

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655

Val Thr Glu Lys His Leu Thr Glu Val Lys Ser Thr Ser
 660 665

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 76
ggaccaggat ccatgaaaat aaaaacaggt

30

<210> 77
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 77
Gly Gly Ser Gly His His His His His His His His
1 5 10

<210> 78
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 78
gctcttctca cccagaaacg ctggtg

26

<210> 79
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 79
ctgattaagc attgggacaa gagccactga agaga

35

<210> 80
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
cacccagaaa cgctggtg

18

<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 81
 ctgattaagc attgggacaa gagc

24

<210> 82
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 82
 gtggctcttg tcccaatgct taatcag

27

<210> 83
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83
 caccagcgtt tctgg

15

<210> 84
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 84
 ctgattaagc attgggacaa gagccaccca gaaacgctgg tg

42

<210> 85
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85

ggatccggcg gtggccaccc agaaacgctg gtg

33

<210> 86

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86

ctgattaagc attggggatc c

21

<210> 87

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87

gatccggcgg tggccacca gaaacgctgg tg

32

<210> 88

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 88

ctgattaagc attggg

16

<210> 89

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 89

gatccccaat gcttaatcag

20

<210> 90
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 90
 caccagcggtt tctgggtggc caccgccg

28

<210> 91
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 91
 ctgattaagc attggggatc cggcgggtggc caccagaaa cgctggtg

48

<210> 92
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 92
 ctgattgctg ctgacgggtg aagagcgctc gaggtctctc cgacgggggt tatgcgttc

59

<210> 93
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 93
 ctgattgctg ctgac

15

<210> 94
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94
gacggggggtt atgcgttc 18

<210> 95
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 95
gaacgcataa ccccc 15

<210> 96
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96
cccgtcagca gcaatcag 18

<210> 97
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 97
ctgattgctg ctgacggg 18

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 98
ctgatcgcta ggagacggcg a

21

<210> 99
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 99
His His His His His His
1 5